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ALIGNMENTS					
RESULT 1					
YTA1_CAEEL	STANDARD;	PRT;	1203 AA.		
ID YTA1_CAEEL					
AC Q11069;					
DT 01-NOV-1997 (Rel. 35, Created)					
DT 16-OCT-2001 (Rel. 40, Last sequence update)					
DT 16-OCT-2001 (Rel. 40, Last annotation update)					
DE Hypothetical protein B0416.1 in chromosome X.					
GN B0416.1.					
OS Caenorhabditis elegans.					
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;					
OC Rhabditidae; Peloderrinae; Caenorhabditis.					
OC NCBI_TaxID=6239;					
RN [1]					
RP SEQUENCE FROM N.A.					
RC STRAIN=Bristol N2;					
RA Favell T;					
RL Submitted (MAR-1995) to the EMBL/GenBank/DBJ databases.					
RN [2]					
RP REVISIONS.					
RA Waterston R.;					
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.					
CC --					
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CC or send an email to license@isb-sib.ch).					
CC --					
DR EMBL; U23516; AAG38884.1; -.					
DR WormPep; B0416.1; CEL19663.					
KW Hypothetical protein.					
SQ SEQUENCE 1203 AA; 136059 MW; 1B96886F827CC206 CRC64;					
Query Match 9.9%; Score 99.5; DB 1; Length 1203;					
Best Local Similarity 27.7%; Pred. No. 0.26;					
Matches 39; Conservative 23; Mismatches 50; Indels 29; Gaps 8;					
QY 6 PPSKAWRASQMMTFFIFLLFFPSFTGVLCTLAI-TIWRUKPSADCFFRGLPLFIHSIY 63					
Db 701 PASQIFFRASRSSLFFALLLFLF--LCTLPVGFVIAASKTPSKSCGPF-GNQSFYFYSVI 756					
QY 64 SWIDTLISTRPGYLLWWVWITYRNLLIGSVHFFF-----LITLIVLITYLYWQIT---EG 112					
Db 757 T---DVLHEN-----LDKT-LVNGIKYSLSPGIIIPVVLISLVLYFIAMVTGLSQAN 806					
QY 113 RKIMRLLHEQLINEGKDKMF 133					
Db 807 QDLSQLMLVER--TEKKKIF 825					
RESULT 2					
YXAM_BACSU STANDARD; PRT; 399 AA.					
ID YXAM_BACSU					

AC	01-NOV-1995 (Rel. 32, Created)	FT	TRANSMEM	131	151	POTENTIAL.
DT	15-JUL-1998 (Rel. 36, Last sequence update)	FT	TRANSMEM	153	173	POTENTIAL.
DT	15-JUN-2002 (Rel. 41, Last annotation update)	FT	TRANSMEM	208	228	POTENTIAL.
DE	Hypothetical protein yxam.	FT	TRANSMEM	242	262	POTENTIAL.
DN	YXAM OR SL4MR.	FT	TRANSMEM	296	316	POTENTIAL.
OS	Bacillus subtilis.	FT	TRANSMEM	335	355	POTENTIAL.
OC	Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.	FT	TRANSMEM	357	377	POTENTIAL.
OX	NCBI_TaxID=1423;	FT	TRANSMEM	399	44746	MW; 94AF8E563222E72 CRC64;
RN	[1]	FT	SEQUENCE FROM N.A.			
RP	STRAIN=168 / BGSC11;	FT	SEQUENCE FROM N.A.			
RC	Yoshida K.-I., Seki S., Fujimura M., Miwa Y., Fujita Y.;	FT	SEQUENCE FROM N.A.			
RX	"Cloning and sequencing of a 36-kb region of the <i>Bacillus subtilis</i> genome between the gnt and iol operons.";	FT	SEQUENCE FROM N.A.			
MEMLINE-96093926; PubMed-7584049;	DNA Res. 2:61-69(1995).	FT	SEQUENCE FROM N.A.			
RT	[2]	FT	REVISIONS.			
RA	Fujita Y., Shibayama T., Ishio I., Aoyama D., Yoshida K.-I.;	FT	Fujita Y., Shibayama T., Ishio I., Aoyama D., Yoshida K.-I.;			
RL	Submitted (JUL-1997) to the EMBL/GenBank/DDBJ databases.	FT	Fujita Y., Shibayama T., Ishio I., Aoyama D., Yoshida K.-I.;			
RN	[3]	FT	SEQUENCE FROM N.A.			
RP	STRAIN=168;	FT	SEQUENCE FROM N.A.			
RX	MEDLINE-9804033; PubMed=9384377;	FT	SEQUENCE FROM N.A.			
RA	Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,	FT	SEQUENCE FROM N.A.			
RA	Azevedo V., Bertero M.G., Bessieres P., Bolctein A., Borchart S.,	FT	SEQUENCE FROM N.A.			
RA	Boriss R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,	FT	SEQUENCE FROM N.A.			
RA	Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,	FT	SEQUENCE FROM N.A.			
RA	Choi S.K., Codani J.J., Conneron I.F., Cummings N.J., Daniel R.A.,	FT	SEQUENCE FROM N.A.			
RA	Denizot F., Devine K.M., Dusterhoff A., Ehrlich S.D., Emmerson P.T.,	FT	SEQUENCE FROM N.A.			
RA	Entian K.D., Errington J., Fabret C., Ferrari E., Foulger D.,	FT	SEQUENCE FROM N.A.			
RA	Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,	FT	SEQUENCE FROM N.A.			
RA	Ghim S.Y., Glaser P., Goffeau A., Golightly E.J., Grandi G.,	FT	SEQUENCE FROM N.A.			
RA	Guiseppi G., Guy B.J., Haga K., Halleck J., Harwood C.R., Renaud A.,	FT	SEQUENCE FROM N.A.			
RA	Hilbert H., Holsappel S., Hosono S., Hullu M.F., Itaya M., Jones L.,	FT	SEQUENCE FROM N.A.			
RA	Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M., Klein C.,	FT	SEQUENCE FROM N.A.			
RA	Kobayashi Y., Koetter P., Konigstein G., Krogh S., Kumano M.,	FT	SEQUENCE FROM N.A.			
RA	Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,	FT	SEQUENCE FROM N.A.			
RA	Lee S.M., Levine A., Liu H., Masuda S., Mauel C., Medigue C.,	FT	SEQUENCE FROM N.A.			
RA	Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,	FT	SEQUENCE FROM N.A.			
RA	Noone D., O'Reilly M., Ogawa K., Ogihara A., Oudega B., Park S.H.,	FT	SEQUENCE FROM N.A.			
RA	Parro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M.,	FT	SEQUENCE FROM N.A.			
RA	Presecan E., Pujic P., Purnelle B., Rapoport G., Rey M., Reynolds S.,	FT	SEQUENCE FROM N.A.			
RA	Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadaie Y.,	FT	SEQUENCE FROM N.A.			
RA	Sato T., Scanlan E., Schleich S., Schroeter R., Scoffone F.,	FT	SEQUENCE FROM N.A.			
RA	Sekiguchi J., Sekowska A., Seror S.J., Seror P., Shin B.S., Soldo B.,	FT	SEQUENCE FROM N.A.			
RA	Sorokin A., Tacconi E., Takeagi T., Takahashi H., Takekumar K.,	FT	SEQUENCE FROM N.A.			
RA	Takeuchi M., Tamakoshi A., Tanaka T., Terpstra P., Tognoni A.,	FT	SEQUENCE FROM N.A.			
RA	Tosato V., Uchiyama S., Vandebbol M., Vannier F., Vassarotti A.,	FT	SEQUENCE FROM N.A.			
RA	Viali A., Wambutt R., Wedler E., Wedler H., Weitzengreger T.,	FT	SEQUENCE FROM N.A.			
RA	Winters P., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yata K.,	FT	SEQUENCE FROM N.A.			
RA	Yoshida K., Yoshikawa H.F., Zumstein E., Yoshikawa H., Danchin A.,	FT	SEQUENCE FROM N.A.			
RT	"The complete genome sequence of the Gram-positive bacterium <i>Bacillus subtilis</i> ."	FT	SEQUENCE FROM N.A.			
RL	Nature 390:249-256(1997).	FT	SEQUENCE FROM N.A.			
CC	-!- SUBCELLULAR LOCATION: Integral membrane protein (Probable).	FT	SEQUENCE FROM N.A.			
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CC	EMBL: AB005554; BAA21592.1; -	FT	SEQUENCE FROM N.A.			
DR	EMBL: 299124; CAB16029.1; -	FT	SEQUENCE FROM N.A.			
DR	Subtilist: BG1115; yxam.	FT	SEQUENCE FROM N.A.			
KW	Hypothetical protein; Transmembrane; Complete proteome.	FT	SEQUENCE FROM N.A.			
FT	TRANSMEM 7 27 POTENTIAL.	FT	SEQUENCE FROM N.A.			
FT	TRANSMEM 33 53 POTENTIAL.	FT	SEQUENCE FROM N.A.			
FT	TRANSMEM 79 99 POTENTIAL.	FT	SEQUENCE FROM N.A.			
FT	TRANSMEM 12 32 POTENTIAL.	FT	SEQUENCE FROM N.A.			
FT	TRANSMEM 131 151 POTENTIAL.	FT	SEQUENCE FROM N.A.			
FT	TRANSMEM 153 173 POTENTIAL.	FT	SEQUENCE FROM N.A.			
FT	TRANSMEM 208 228 POTENTIAL.	FT	SEQUENCE FROM N.A.			
FT	TRANSMEM 242 262 POTENTIAL.	FT	SEQUENCE FROM N.A.			
FT	TRANSMEM 296 316 POTENTIAL.	FT	SEQUENCE FROM N.A.			
FT	TRANSMEM 335 355 POTENTIAL.	FT	SEQUENCE FROM N.A.			
FT	TRANSMEM 357 377 POTENTIAL.	FT	SEQUENCE FROM N.A.			
FT	TRANSMEM 399 AA; 44746 MW; 94AF8E563222E72 CRC64;	FT	SEQUENCE FROM N.A.			
FT	Query Match 8.4%; Score 84; DB 1; Length 399;	FT	SEQUENCE FROM N.A.			
FT	Best Local Similarity 19.9%; Pred. No. 2;	FT	SEQUENCE FROM N.A.			
FT	Matches 35; Conservative 31; Mismatches 48; Indels 62; Gaps 8;	FT	SEQUENCE FROM N.A.			
FT	QY 4 FOPPSKAW----RASQMMFFIFLL--FFPSF-TGVLCIATIWRLKPSADCGPFR 53	FT	SEQUENCE FROM N.A.			
Db	50 FEVPSGVFAFDYRGKISIASSFFSILTWAFFPFDISAATCILMIIWALSDLSIGSF 109	FT	SEQUENCE FROM N.A.			
FT	QY 54 GLPLFIHSIYSWIDL-----STRPGYLWVWVWYRNLL 141	FT	SEQUENCE FROM N.A.			
Db	110 -----TWMRSRAGEDRFGKEMMKNTQLLHQIINEG----KDKMFLIEKLKL 152	FT	SEQUENCE FROM N.A.			
FT	QY 90 HFFFILFTLVLITYLWQOTEGRKIMRLHQEIQINEG---- 152	FT	SEQUENCE FROM N.A.			
Db	153 -FPFLLVWVIVLLEFW----MSVFIKVPVSSETNHGDQNDQHDSIKIKESLKI 201	FT	SEQUENCE FROM N.A.			
FT	OX Y38A_MYCGE STANDARD; PRT; 149 AA.	FT	SEQUENCE FROM N.A.			
FT	RESULT 3	FT	SEQUENCE FROM N.A.			
FT	ID Y38A_MYCGE	FT	SEQUENCE FROM N.A.			
FT	AC 09ZB71;	FT	SEQUENCE FROM N.A.			
FT	DT 30-MAY-2000 (Rel. 39, Created)	FT	SEQUENCE FROM N.A.			
FT	DT 30-MAY-2000 (Rel. 39, Last sequence update)	FT	SEQUENCE FROM N.A.			
FT	DT 16-OCT-2001 (Rel. 40, Last annotation update)	FT	SEQUENCE FROM N.A.			
FT	DE Hypothetical protein MG384.1.	FT	SEQUENCE FROM N.A.			
FT	GN MG384.1.	FT	SEQUENCE FROM N.A.			
FT	OS Mycoplasma genitalium.	FT	SEQUENCE FROM N.A.			
FT	OC Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.	FT	SEQUENCE FROM N.A.			
FT	OX NCBI_TaxID=2097;	FT	SEQUENCE FROM N.A.			
FT	RP SEQUENCE FROM N.A.	FT	SEQUENCE FROM N.A.			
FT	RC STRAIN=ATCC 33530 / G-37;	FT	SEQUENCE FROM N.A.			
FT	RX MEDLINE-96026346; PubMed=7569993;	FT	SEQUENCE FROM N.A.			
FT	RA Fraser C.M., Gocayne J.D., White O., Adams M.D., Clayton R.A.,	FT	SEQUENCE FROM N.A.			
FT	RA Fleischmann R.D., Bult C.J., Kerlavage A.R., Sutton G., Kelley J.M.,	FT	SEQUENCE FROM N.A.			
FT	RA Fritchman J.L., Weidman J.F., Small K.V., Sandusky M., Fuhrmann J.L.,	FT	SEQUENCE FROM N.A.			
FT	RA Nguyen D.T., Utterback T.R., Sauder D.M., Phillips C.A., Merrick J.M.,	FT	SEQUENCE FROM N.A.			
FT	RA Tomb J.-F., Dougherty B.A., Bott K.F., Hu P.-C., Lucier T.S.,	FT	SEQUENCE FROM N.A.			
FT	RA Peterson S.N., Smith H.O., Hutchinson C.A. III, Venter J.C.,	FT	SEQUENCE FROM N.A.			
FT	RA "The minimal gene complement of Mycoplasma genitalium.";	FT	SEQUENCE FROM N.A.			
FT	RT Science 270:397-403(1995).	FT	SEQUENCE FROM N.A.			
FT	RL "The minimal gene complement of Mycoplasma genitalium.";	FT	SEQUENCE FROM N.A.			
FT	RN [2]	FT	SEQUENCE FROM N.A.			
FT	FT IDENTIFICATION.	FT	SEQUENCE FROM N.A.			
FT	RA Fraser C.M., Gocayne J.D., White O., Adams M.D., Clayton R.A.,	FT	SEQUENCE FROM N.A.			
FT	RA Fleischmann R.D., Bult C.J., Kerlavage A.R., Sutton G., Kelley J.M.,	FT	SEQUENCE FROM N.A.			
FT	RA Fritchman J.L., Weidman J.F., Small K.V., Sandusky M., Fuhrmann J.L.,	FT	SEQUENCE FROM N.A.			
FT	RA Nguyen D.T., Utterback T.R., Sauder D.M., Phillips C.A., Merrick J.M.,	FT	SEQUENCE FROM N.A.			
FT	RA Tomb J.-F., Dougherty B.A., Bott K.F., Hu P.-C., Lucier T.S.,	FT	SEQUENCE FROM N.A.			
FT	RA Peterson S.N., Smith H.O., Hutchinson C.A. III, Venter J.C.,	FT	SEQUENCE FROM N.A.			
FT	RA Submitted (OCT-1998) to the EMBL/GenBank/DDBJ databases.	FT	SEQUENCE FROM N.A.			
FT	CC -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).	FT	SEQUENCE FROM N.A.			
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CC	EMBL: AB005554; BAA21592.1; -	FT	SEQUENCE FROM N.A.			
CC	EMBL: 299124; CAB16029.1; -	FT	SEQUENCE FROM N.A.			
CC	Subtilist: BG1115; yxam.	FT	SEQUENCE FROM N.A.			
CC	Hypothetical protein; Transmembrane; Complete proteome.	FT	SEQUENCE FROM N.A.			
CC	TRANSMEM 7 27 POTENTIAL.	FT	SEQUENCE FROM N.A.			
CC	TRANSMEM 33 53 POTENTIAL.	FT	SEQUENCE FROM N.A.			
CC	TRANSMEM 79 99 POTENTIAL.	FT	SEQUENCE FROM N.A.			

CC	PIR; A38908; A38908;	DR	DR	
CC	InterPro; IPR002066; Bac_export_2;	DR	InterPro; IPR002066; Bac_export_2;	
CC	Pfam; PF01312; Bac_export_2;	DR	Pfam; PF01312; Bac_export_2;	
CC	PRINTS; PRO0950; TYPE3IMSPROT;	DR	PRINTS; PRO0950; TYPE3IMSPROT;	
KW	Virulence; Transmembrane; Inner membrane; Plasmid.	DR	Virulence; Transmembrane; Inner membrane; Plasmid.	
FT	TRANSMEM 28	DR	TRANSMEM 28	
FT	TRANSMEM 70	DR	TRANSMEM 70	
FT	POTENTIAL.	DR	POTENTIAL.	
FT	TRANSMEM 133	DR	TRANSMEM 133	
FT	POTENTIAL.	DR	POTENTIAL.	
FT	TRANSMEM 158	DR	TRANSMEM 158	
FT	POTENTIAL.	DR	POTENTIAL.	
FT	TRANSMEM 181	DR	TRANSMEM 181	
FT	POTENTIAL.	DR	POTENTIAL.	
SQ	SEQUENCE 260 AA; 39852 MW; 48BBB531BFE034BC CRC64;	DR	SEQUENCE 342 AA; 39852 MW; 48BBB531BFE034BC CRC64;	
Query Match	7.7%; Score 77; DB 1; Length 342;	DR	Query Match	7.7%; Score 77; DB 1; Length 342;
Best Local Similarity	22.9%; Pred. No. 7.2;	DR	Best Local Similarity	22.9%; Pred. No. 7.2;
Matches	44; Conservative 31; Mismatches 43; Indels 74; Gaps 11;	DR	Matches	44; Conservative 31; Mismatches 43; Indels 74; Gaps 11;
QY	22 FLLEFPSTFGVLCTAITIWRKPSA-----DCGPFRLPLFIHSIYWSWIDTLSTRGY 75	DR	QY	22 FLLEFPSTFGVLCTAITIWRKPSA-----DCGPFRLPLFIHSIYWSWIDTLSTRGY 75
Db	83 FPLFFCVCVLASAVLPTLVQTKFVLAIAKIDFESVLPNVKGL---KKIFS----- 127	DR	Db	83 FPLFFCVCVLASAVLPTLVQTKFVLAIAKIDFESVLPNVKGL---KKIFS----- 127
QY	76 LWVWVWVYRNLLIGSWHFFF--ILTLILVL-LITYLYWQITEGRKIMIRLHEQIINEG--- 128	DR	QY	76 LWVWVWVYRNLLIGSWHFFF--ILTLILVL-LITYLYWQITEGRKIMIRLHEQIINEG--- 128
Db	128 -----IKTIKEFFKSILLIILALITYFWF--INDRKITIFSQFSSV--DGLYLI 173	DR	Db	128 -----IKTIKEFFKSILLIILALITYFWF--INDRKITIFSQFSSV--DGLYLI 173
QY	129 -----KDKM-----FLIEKLIKQLQDMEKKANPSSLVLERREVEQQGFLHLIG 169	DR	QY	129 -----KDKM-----FLIEKLIKQLQDMEKKANPSSLVLERREVEQQGFLHLIG 169
Db	174 WGRLFKLILFLAFASILWILDFVIERFLYMKDM-----MMDKQEIKREYI---- 220	DR	Db	174 WGRLFKLILFLAFASILWILDFVIERFLYMKDM-----MMDKQEIKREYI---- 220
QY	170 EHDGSLDLRSRR 181	DR	QY	170 EHDGSLDLRSRR 181
Db	221 EQEGHFFETKSRR 232	DR	Db	221 EQEGHFFETKSRR 232
RESULT 6		DR	RESULT 6	
YEDQ_ECO57		DR	YEDQ_ECO57	
ID YEDQ_ECO57	STANDARD; PRT; 564 AA.	DR	ID YEDQ_ECO57	STANDARD; PRT; 564 AA.
AC Q8X892;		DR	AC Q8X892;	
AC	15-JUN-2002 (Rel. 41, Created)	DR	AC	15-JUN-2002 (Rel. 41, Created)
DT	15-JUN-2002 (Rel. 41, Last sequence update)	DR	DT	15-JUN-2002 (Rel. 41, Last sequence update)
DE	Hypothetical protein YedQ.	DR	DE	Hypothetical protein YedQ.
GN YEDQ OR Z3047 OR ECS2694.		DR	GN YEDQ OR Z3047 OR ECS2694.	
OS Escherichia coli 0157:H7.		DR	OS Escherichia coli 0157:H7.	
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;		DR	OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;	
OC Escherichia.		DR	OC Escherichia.	
OX NCBI_TaxID=833334;		DR	OX NCBI_TaxID=833334;	
RN [1]		DR	RN [1]	
RP SEQUENCE FROM N.A.		DR	RP SEQUENCE FROM N.A.	
RC STRAIN=O157:H7 / RIMD 0509952;		DR	RC STRAIN=O157:H7 / RIMD 0509952;	
RX MEDLINE=21074935; PubMed=11205551;		DR	RX MEDLINE=21074935; PubMed=11205551;	
RA Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,		DR	RA Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,	
RA Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,		DR	RA Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,	
RA Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,		DR	RA Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,	
RA Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamitis K.,		DR	RA Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamitis K.,	
RA Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,		DR	RA Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,	
RA Welch R.A., Blattner F.R.;		DR	RA Welch R.A., Blattner F.R.;	
RT "Genome sequence of enterohaemorrhagic Escherichia coli 0157:H7.";		DR	RT "Genome sequence of enterohaemorrhagic Escherichia coli 0157:H7.";	
RL Nature 409:529-533 (2001).		DR	RL Nature 409:529-533 (2001).	
RN [2]		DR	RN [2]	
RP SEQUENCE FROM N.A.		DR	RP SEQUENCE FROM N.A.	
RC STRAIN=O157:H7 / RIMD 0509952;		DR	RC STRAIN=O157:H7 / RIMD 0509952;	
RX MEDLINE=21156231; PubMed=11258796;		DR	RX MEDLINE=21156231; PubMed=11258796;	
RA Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K.,		DR	RA Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K.,	
RA Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,		DR	RA Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,	
RA Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T.,		DR	RA Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T.,	
RA Kuhara S., Shiba T., Hattori M., Shinagawa H.;		DR	RA Kuhara S., Shiba T., Hattori M., Shinagawa H.;	
RT "Complete genome sequence of enterohaemorrhagic Escherichia coli 0157:H7 and genomic comparison with a laboratory strain K-12.";		DR	RT "Complete genome sequence of enterohaemorrhagic Escherichia coli 0157:H7 and genomic comparison with a laboratory strain K-12.";	
DNA Res. 8:11-22 (2001).		DR	DNA Res. 8:11-22 (2001).	
-1 - SUBCELLULAR LOCATION: Integral membrane protein (Potential).		DR	-1 - SUBCELLULAR LOCATION: Integral membrane protein (Potential).	
-1 - SIMILARITY: BELONGS TO THE YATC / YFIN (E.COLI), YHCK (B.SUBTILIS)		DR	-1 - SIMILARITY: BELONGS TO THE YATC / YFIN (E.COLI), YHCK (B.SUBTILIS)	
CC FAMILY.		DR	CC FAMILY.	
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CC	EMBL; A0005417; AAG56970.1; -.	DR	CC	EMBL; A0005417; AAG56970.1; -.
CC	InterPro; IPR000160; GGDEF.	DR	CC	InterPro; IPR000160; GGDEF.
CC	Pfam; PF00990; GGDEF; 1.	DR	CC	Pfam; PF00990; GGDEF; 1.
CC	SMART; SM0267; DUF1; 1.	DR	CC	SMART; SM0267; DUF1; 1.
CC	TIGRFAMS; TIGR00254; GGDEF; 1.	DR	CC	TIGRFAMS; TIGR00254; GGDEF; 1.
CC	Hypothetical protein; Transmembrane; Complete proteome.	DR	CC	Hypothetical protein; Transmembrane; Complete proteome.
FT	TRANSMEM 20	DR	FT	TRANSMEM 20
FT	POTENTIAL.	DR	FT	POTENTIAL.
SQ	SEQUENCE 564 AA; 64287 MW; BEBC2286ADBAECB0 CRC64;	DR	SQ	SEQUENCE 564 AA; 64287 MW; BEBC2286ADBAECB0 CRC64;
Query Match	7.7%; Score 77; DB 1; Length 564;	DR	Query Match	7.7%; Score 77; DB 1; Length 564;
Best Local Similarity	26.0%; Pred. No. 13;	DR	Best Local Similarity	26.0%; Pred. No. 13;
Matches	38; Conservative 25; Mismatches 43; Indels 40; Gaps 8;	DR	Matches	38; Conservative 25; Mismatches 43; Indels 40; Gaps 8;
QY	64 SWIDTLSTR--PGYLMWVWVYRNLLIGSWHFFFILTLIVLITYLYWQ--ITBGRKIMIR 118	DR	QY	64 SWIDTLSTR--PGYLMWVWVYRNLLIGSWHFFFILTLIVLITYLYWQ--ITBGRKIMIR 118
Db	11 SWLKKLARRLGPGH-----VNLCFI--VVLFLSTLTLWREVVVLVEDAYISSQ 56	DR	Db	11 SWLKKLARRLGPGH-----VNLCFI--VVLFLSTLTLWREVVVLVEDAYISSQ 56
QY	119 LLHEQIINEGDKK--MFELIEKLIKQLQDMEKKA---NPSSLVLERREVEQQGFLHLGEH 171	DR	QY	119 LLHEQIINEGDKK--MFELIEKLIKQLQDMEKKA---NPSSLVLERREVEQQGFLHLGEH 171
Db	57 RNHLENVANALDKHLOQYVNVKLFLLRNGMREALVAPLDFTSLRDAYTEFEO---HRDEH 112	DR	Db	57 RNHLENVANALDKHLOQYVNVKLFLLRNGMREALVAPLDFTSLRDAYTEFEO---HRDEH 112
QY	172 DGSIDLRSRS-----VOEGN 187	DR	QY	172 DGSIDLRSRS-----VOEGN 187
Db	113 AWQIELNRRRTLSVNGVSDALVSEG 138	DR	Db	113 AWQIELNRRRTLSVNGVSDALVSEG 138
RESULT 7		DR	RESULT 7	
T2N5_NOSS7		DR	T2N5_NOSS7	
ID T2N5_NOSS7	STANDARD; PRT; 220 AA.	DR	ID T2N5_NOSS7	STANDARD; PRT; 220 AA.
AC P35677;		DR	AC P35677;	
DT 01-JUN-1994 (Rel. 29, Created)		DR	DT 01-JUN-1994 (Rel. 29, Created)	
DT 01-JUN-1994 (Rel. 29, Last sequence update)		DR	DT 01-JUN-1994 (Rel. 29, Last sequence update)	
DT 16-OCT-2001 (Rel. 40, Last annotation update)		DR	DT 16-OCT-2001 (Rel. 40, Last annotation update)	
DE Type II restriction enzyme NspV (EC 3.1.21.4) (Endonuclease NspV).		DR	DE Type II restriction enzyme NspV (EC 3.1.21.4) (Endonuclease NspV).	
DE (R.NspV).		DR	DE (R.NspV).	
GN NspV.		DR	GN NspV.	
OS Nostoc sp. (strain PCC 7524).		DR	OS Nostoc sp. (strain PCC 7524).	
OC Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc.		DR	OC Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc.	
OX NCBI_TaxID=28072;		DR	OX NCBI_TaxID=28072;	
RN [1]		DR	RN [1]	
RP SEQUENCE FROM N.A.		DR	RP SEQUENCE FROM N.A.	
RC MEDLINE=93376523; PubMed=8367311;		DR	RC MEDLINE=93376523; PubMed=8367311;	
RX Ueno T., Ito H., Kotani H., Nakajima K.; "Cloning and expression of the NspV restriction-modification genes of Nostoc sp. strain PCC7524." Nucleic Acids Res. 21:3899-3899(1993).		DR	RX Ueno T., Ito H., Kotani H., Nakajima K.; "Cloning and expression of the NspV restriction-modification genes of Nostoc sp. strain PCC7524." Nucleic Acids Res. 21:3899-3899(1993).	
RA	-1 - FUNCTION: RECOGNIZES THE DOUBLE-STRANDED SEQUENCE TTCCGA AND CLEAVES AFTER T-2.	DR	RA	-1 - FUNCTION: RECOGNIZES THE DOUBLE-STRANDED SEQUENCE TTCCGA AND CLEAVES AFTER T-2.
CC	specific double-stranded fragments with terminal 5'-phosphates.	DR	CC	specific double-stranded fragments with terminal 5'-phosphates.
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).	DR	CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).
CC	EMBL; D14719; BAA03538.1; -.	DR	CC	EMBL; D14719; BAA03538.1; -.
CC	Hydrolase; Endonuclease; Nuclease; Restriction system.	DR	CC	Hydrolase; Endonuclease; Nuclease; Restriction system.
KW		DR	KW	

SQ	SEQUENCE	220 AA;	24604 MW;	BA38B9644794BBC6 CRC64;	DR	TIGRFAMS; TIGR00254; GGDEF; 1.
Query Match		7.6%	Score 76.5;	DB 1;	KW	Hypothetical protein; Transmembrane; Complete proteome.
Best Local Similarity		23.3%	Pred. No. 4.9;	Length 220;	FT	POTENTIAL.
Matches		42;	Conservative	34;	TRANSMEM	20
QY	29	FTGVLCLTAITIWRKPSADCGRPFRGLPLFIHSIYSWIDTISTRPGYLWVWVYRLIGS 88	59;	Indels 45;	40	POTENTIAL.
Db	66	FPGILVWDVKTISR-QPQSSC-PFKSAROKIFGL-----GYSILIFVYDKIDNS 112	11;	Gaps 11;	SEQUENCE	380
QY	89	VHFFFLTILVILITLYWQITEGRKIMIRLHQIINEG-KDKM--FLIEKLKLQDME 145	11;	Best Local Similarity 26.0%;	38;	Conservative 25;
Db	113	TN--RTATLNILHTIVSAERTADFQ-MTRGIRNLANEGKDDLIAFMSDRNLPVDEIE 169	43;	Mismatches 43;	SEQUENCE	40
QY	146	KKANPSSLVLERREVEQQGFLHL-----GEHDGSDLRSRRSQQEGNP 188	59;	Indels 40;	DR	Gaps 8;
Db	170	-AGNVAAILL--RNPPMOMGFLTISNALQWRLQYGRVIERAGQEDGIL-----TVYRNRP 220	11;	Gaps 11;	SEQUENCE	380
RESULT 8						
YEDQ_ECOLI						
ID		YEDQ_ECOLI	STANDARD;			
AC		P76330; P94746;	PRT;	564 AA.		
DT		15-JUN-2002 (Rel. 41, Created)				
DT		15-JUN-2002 (Rel. 41, Last sequence update)				
DE		Hypothetical protein yedQ.				
GN		YEDQ OR B1956.				
OS		Escherichia coli.				
OC		Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;				
OC		Escherichia.				
OX		NCBI_TAXID=562;				
RN		[1]				
RP		SEQUENCE FROM N.A.				
RC		STRAIN=K12 / MG1655;				
RX		MEDLINE=97246617; PubMed=9278503;				
RA		Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,				
RA		Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,				
RA		Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,				
RA		Mau B., Shao Y.;				
RT		"The complete genome sequence of Escherichia coli K-12. ";				
RT		Science 277:1453-1474 (1997).				
RN		[2]				
RP		SEQUENCE FROM N.A.				
RC		STRAIN=K12;				
RX		MEDLINE=97251358; PubMed=9097040;				
RA		Itoh T., Aiba H., Baba T., Fujita K., Hayashi K., Inada T., Isono K.,				
RA		Kasai H., Kimura S., Kitakawa M., Makino K., Miki T.,				
RA		Mizobuchi K., Mori H., Mori T., Motomura K., Nakade S., Nakamura Y.,				
RA		Nishimoto H., Nishio Y., Oshima T., Saito N., Sampei G., Seki Y.,				
RA		Sivasundaram S., Tagami H., Takeda J., Takemoto K., Wada C.,				
RA		Yamamoto Y., Horiuchi T.;				
RT		"A 460-kb DNA Sequence of the Escherichia coli K-12 Genome Corresponding to the 40.1-50.0 min Region on the Linkage Map. ";				
RT		DNA Res. 3:379-392(1996).				
RL		-- SUBCELLULAR LOCATION: Integral membrane protein.				
CC		-- SIMILARITY: BELONGS TO THE CATION TRANSPORT ATPASES FAMILY				
CC		FAMILY.				
CC		-----				
CC		This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).				
CC		-----				
CC		DR EMBL; AE00287; AAC75022.1; ALT_INIT.				
CC		DR EMBL; D90835; BAA15784.1; -.				
CC		DR ECOGENE; EG14040; YedQ.				
CC		DR InterPro; IPR00160; GGDEF.				
CC		DR Pfam; PF00990; GGDEF; 1.				
CC		DR SMART; SM00267; DUF1; 1.				
DR		-----				
DR		DR TIGRFAMS; TIGR00254; GGDEF; 1.				
FT		KW HYPOTHETICAL PROTEIN; TRANSMEMBRANE; COMPLETE PROTEOME.				
FT		FT TRANSMEM 20 40 POTENTIAL.				
FT		FT TRANSMEM 360 380 POTENTIAL.				
FT		FT SEQUENCE 564 AA; 64283 MW; 05FB02C1BE2A8938 CRC64;				
FT		-----				
FT		Query Match 7.6%;	Score 76;	DB 1;	DR TIGRFAMS; TIGR00254; GGDEF; 1.	
FT		Best Local Similarity 26.0%;	Pred. No. 15;	Length 564;	KW HYPOTHETICAL PROTEIN; TRANSMEMBRANE; COMPLETE PROTEOME.	
FT		Matches 38;	Conservative 25;	Mismatches 43;	FT TRANSMEM 20 40 POTENTIAL.	
FT		-----				
FT		Query Match 7.6%;	Score 76;	DB 1;	DR TIGRFAMS; TIGR00254; GGDEF; 1.	
FT		Best Local Similarity 26.0%;	Pred. No. 15;	Length 564;	KW HYPOTHETICAL PROTEIN; TRANSMEMBRANE; COMPLETE PROTEOME.	
FT		Matches 38;	Conservative 25;	Mismatches 43;	FT TRANSMEM 20 40 POTENTIAL.	
FT		-----				
FT		Query Match 7.6%;	Score 76;	DB 1;	DR TIGRFAMS; TIGR00254; GGDEF; 1.	
FT		Best Local Similarity 26.0%;	Pred. No. 15;	Length 564;	KW HYPOTHETICAL PROTEIN; TRANSMEMBRANE; COMPLETE PROTEOME.	
FT		Matches 38;	Conservative 25;	Mismatches 43;	FT TRANSMEM 20 40 POTENTIAL.	
FT		-----				
FT		Query Match 7.6%;	Score 76;	DB 1;	DR TIGRFAMS; TIGR00254; GGDEF; 1.	
FT		Best Local Similarity 26.0%;	Pred. No. 15;	Length 564;	KW HYPOTHETICAL PROTEIN; TRANSMEMBRANE; COMPLETE PROTEOME.	
FT		Matches 38;	Conservative 25;	Mismatches 43;	FT TRANSMEM 20 40 POTENTIAL.	
FT		-----				
FT		Query Match 7.6%;	Score 76;	DB 1;	DR TIGRFAMS; TIGR00254; GGDEF; 1.	
FT		Best Local Similarity 26.0%;	Pred. No. 15;	Length 564;	KW HYPOTHETICAL PROTEIN; TRANSMEMBRANE; COMPLETE PROTEOME.	
FT		Matches 38;	Conservative 25;	Mismatches 43;	FT TRANSMEM 20 40 POTENTIAL.	
FT		-----				
FT		Query Match 7.6%;	Score 76;	DB 1;	DR TIGRFAMS; TIGR00254; GGDEF; 1.	
FT		Best Local Similarity 26.0%;	Pred. No. 15;	Length 564;	KW HYPOTHETICAL PROTEIN; TRANSMEMBRANE; COMPLETE PROTEOME.	
FT		Matches 38;	Conservative 25;	Mismatches 43;	FT TRANSMEM 20 40 POTENTIAL.	
FT		-----				
FT		Query Match 7.6%;	Score 76;	DB 1;	DR TIGRFAMS; TIGR00254; GGDEF; 1.	
FT		Best Local Similarity 26.0%;	Pred. No. 15;	Length 564;	KW HYPOTHETICAL PROTEIN; TRANSMEMBRANE; COMPLETE PROTEOME.	
FT		Matches 38;	Conservative 25;	Mismatches 43;	FT TRANSMEM 20 40 POTENTIAL.	
FT		-----				
FT		Query Match 7.6%;	Score 76;	DB 1;	DR TIGRFAMS; TIGR00254; GGDEF; 1.	
FT		Best Local Similarity 26.0%;	Pred. No. 15;	Length 564;	KW HYPOTHETICAL PROTEIN; TRANSMEMBRANE; COMPLETE PROTEOME.	
FT		Matches 38;	Conservative 25;	Mismatches 43;	FT TRANSMEM 20 40 POTENTIAL.	
FT		-----				
FT		Query Match 7.6%;	Score 76;	DB 1;	DR TIGRFAMS; TIGR00254; GGDEF; 1.	
FT		Best Local Similarity 26.0%;	Pred. No. 15;	Length 564;	KW HYPOTHETICAL PROTEIN; TRANSMEMBRANE; COMPLETE PROTEOME.	
FT		Matches 38;	Conservative 25;	Mismatches 43;	FT TRANSMEM 20 40 POTENTIAL.	
FT		-----				
FT		Query Match 7.6%;	Score 76;	DB 1;	DR TIGRFAMS; TIGR00254; GGDEF; 1.	
FT		Best Local Similarity 26.0%;	Pred. No. 15;	Length 564;	KW HYPOTHETICAL PROTEIN; TRANSMEMBRANE; COMPLETE PROTEOME.	
FT		Matches 38;	Conservative 25;	Mismatches 43;	FT TRANSMEM 20 40 POTENTIAL.	
FT		-----				
FT		Query Match 7.6%;	Score 76;	DB 1;	DR TIGRFAMS; TIGR00254; GGDEF; 1.	
FT		Best Local Similarity 26.0%;	Pred. No. 15;	Length 564;	KW HYPOTHETICAL PROTEIN; TRANSMEMBRANE; COMPLETE PROTEOME.	
FT		Matches 38;	Conservative 25;	Mismatches 43;	FT TRANSMEM 20 40 POTENTIAL.	
FT		-----				
FT		Query Match 7.6%;	Score 76;	DB 1;	DR TIGRFAMS; TIGR00254; GGDEF; 1.	
FT		Best Local Similarity 26.0%;	Pred. No. 15;	Length 564;	KW HYPOTHETICAL PROTEIN; TRANSMEMBRANE; COMPLETE PROTEOME.	
FT		Matches 38;	Conservative 25;	Mismatches 43;	FT TRANSMEM 20 40 POTENTIAL.	
FT		-----				
FT		Query Match 7.6%;	Score 76;	DB 1;	DR TIGRFAMS; TIGR00254; GGDEF; 1.	
FT		Best Local Similarity 26.0%;	Pred. No. 15;	Length 564;	KW HYPOTHETICAL PROTEIN; TRANSMEMBRANE; COMPLETE PROTEOME.	
FT		Matches 38;	Conservative 25;	Mismatches 43;	FT TRANSMEM 20 40 POTENTIAL.	
FT		-----				
FT		Query Match 7.6%;	Score 76;	DB 1;	DR TIGRFAMS; TIGR00254; GGDEF; 1.	
FT		Best Local Similarity 26.0%;	Pred. No. 15;	Length 564;	KW HYPOTHETICAL PROTEIN; TRANSMEMBRANE; COMPLETE PROTEOME.	
FT		Matches 38;	Conservative 25;	Mismatches 43;	FT TRANSMEM 20 40 POTENTIAL.	
FT		-----				
FT		Query Match 7.6%;	Score 76;	DB 1;	DR TIGRFAMS; TIGR00254; GGDEF; 1.	
FT		Best Local Similarity 26.0%;	Pred. No. 15;	Length 564;	KW HYPOTHETICAL PROTEIN; TRANSMEMBRANE; COMPLETE PROTEOME.	
FT		Matches 38;	Conservative 25;	Mismatches 43;	FT TRANSMEM 20 40 POTENTIAL.	
FT		-----				
FT		Query Match 7.6%;	Score 76;	DB 1;	DR TIGRFAMS; TIGR00254; GGDEF; 1.	
FT		Best Local Similarity 26.0%;	Pred. No. 15;	Length 564;	KW HYPOTHETICAL PROTEIN; TRANSMEMBRANE; COMPLETE PROTEOME.	
FT		Matches 38;	Conservative 25;	Mismatches 43;	FT TRANSMEM 20 40 POTENTIAL.	
FT		-----				
FT		Query Match 7.6%;	Score 76;	DB 1;	DR TIGRFAMS; TIGR00254; GGDEF; 1.	
FT		Best Local Similarity 26.0%;	Pred. No. 15;	Length 564;	KW HYPOTHETICAL PROTEIN; TRANSMEMBRANE; COMPLETE PROTEOME.	
FT		Matches 38;	Conservative 25;	Mismatches 43;	FT TRANSMEM 20 40 POTENTIAL.	
FT		-----				
FT		Query Match 7.6%;	Score 76;	DB 1;	DR TIGRFAMS; TIGR00254; GGDEF; 1.	
FT		Best Local Similarity 26.0%;	Pred. No. 15;	Length 564;	KW HYPOTHETICAL PROTEIN; TRANSMEMBRANE; COMPLETE PROTEOME.	
FT		Matches 38;	Conservative 25;	Mismatches 43;	FT TRANSMEM 20 40 POTENTIAL.	
FT		-----				
FT		Query Match 7.6%;	Score 76;	DB 1;	DR TIGRFAMS; TIGR00254; GGDEF; 1.	
FT		Best Local Similarity 26.0%;	Pred. No. 15;	Length 564;	KW HYPOTHETICAL PROTEIN; TRANSMEMBRANE; COMPLETE PROTEOME.	
FT		Matches 38;	Conservative 25;	Mismatches 43;	FT TRANSMEM 20 40 POTENTIAL.	
FT		-----				
FT		Query Match 7.6%;	Score 76;	DB 1;	DR TIGRFAMS; TIGR00254; GGDEF; 1.	
FT		Best Local Similarity 26.0%;	Pred. No. 15;	Length 564;	KW HYPOTHETICAL PROTEIN; TRANSMEMBRANE; COMPLETE PROTEOME.	
FT		Matches 38;	Conservative 25;	Mismatches 43;	FT TRANSMEM 20 40 POTENTIAL.	
FT		-----				
FT		Query Match 7.6%;	Score 76;	DB 1;	DR TIGRFAMS; TIGR00254; GGDEF; 1.	
FT		Best Local Similarity 26.0%;	Pred. No. 15;	Length 564;	KW HYPOTHETICAL PROTEIN; TRANSMEMBRANE; COMPLETE PROTEOME.	
FT		Matches 38;	Conservative 25;	Mismatches 43;	FT TRANSMEM 20 40 POTENTIAL.	
FT		-----				
FT		Query Match 7.6%;	Score 76;	DB 1;	DR TIGRFAMS; TIGR00254; GGDEF; 1.	
FT		Best Local Similarity 26.0%;	Pred. No. 15;	Length 564;	KW HYPOTHETICAL PROTEIN; TRANSMEMBRANE; COMPLETE PROTEOME.	
FT		Matches				

FT REPEAT 335 358 LRR 10.
 FT REPEAT 359 384 LRR 11.
 FT REPEAT 386 411 LRR 12.
 FT REPEAT 412 436 LRR 13.
 FT REPEAT 412 436 LRR 13.
 FT REPEAT 438 456 LRR 14.
 FT REPEAT 457 476 LRR 15.
 FT REPEAT 477 499 LRR 16.
 FT REPEAT 501 521 LRR 17.
 FT REPEAT 523 546 LRR 18.
 FT DOMAIN 639 784 TIR.
 FT CARBOHYD 114 114 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 199 199 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 442 442 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 784 AA; 90204 MW; 59FDB9DFA7984C18 CRC64;
 Query Match 7.5%; Score 75; DB 1; Length 784;
 Best Local Similarity 23.0%; Pred. No. 28; Mismatches 58; Indels 70; Gaps 11;
 Matches 45; Conservative 23; Mismatches 58; Indels 70; Gaps 11;
 RX MEDLINE-20531768; PubMed-11081518;
 RA Xu Y., Tao X., Shen B., Horng T., Medzhitov R., Manley J.L., Tong L.;
 RT "Structural basis for signal transduction by the Toll/interleukin-1 receptor domains.";
 RL Nature 408:111-115(2000).
 CC -1- FUNCTION: Cooperates with MD-2 to mediate the innate immune response to bacterial lipoproteins and other microbial cell wall components. Acts via Myd88 and TRAF6, leading to NF-kappa-B activation, cytokine secretion and the inflammatory response. May also promote apoptosis in response to lipoproteins. Recognizes mycoplasmal macrophage-activating lipoprotein-2kD (MALP-2), soluble tuberculosis factor (STF), phenol-soluble modulin (PSM) and B.burgdorferi outer surface protein A lipoprotein (OSPA-L)
 CC -1- SUBUNIT: Binds MD-2 and TLR6 via the extracellular domain. Binds Myd88 via their respective TIR domains.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
 CC -1- TISSUE SPECIFICITY: Highly expressed in peripheral blood leukocytes, in particular in monocytes, in bone marrow, lymph node and in spleen. Also detected in lung and in fetal liver. Levels are low in other tissues.
 CC -1- PTM: N-glycosylation (By similarity).
 CC -1- SIMILARITY: BELONGS TO THE TOLL-LIKE RECEPTOR FAMILY.
 CC -1- SIMILARITY: CONTAINS 1 TIR DOMAIN.
 CC -1- SIMILARITY: CONTAINS 14 LEUCINE-RICH REPEATS (LRR).
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 CC
 DR EMBL; AF051152; AAC34377; -.
 DR EMBL; U88878; AAC34133; -.
 DR Genew; HGNC:11848; TLR2.
 DR MIM: 603028; -.
 DR PDB; 1FYW; 22-NOV-00.
 DR InterPro; IPR001611; LRR.
 DR InterPro; IPR00483; LRR_Ctein.
 DR InterPro; IPR003591; LRR_TYP.
 DR InterPro; IPR000157; TIR_domain.
 DR Pfam; PF00560; LRR; 6.
 DR Pfam; PF01463; LRR; 1.
 DR Pfam; PF01582; TIR; 1.
 DR SMART; SM00082; LRRCT; 1.
 DR SMART; SM00369; LRR_TYP; 2.
 DR SMART; SM00255; TIR; 1.
 DR PROSITE; PS50104; TIR; 1.
 DR Receptor; Immune response; Inflammatory response; Signal; Transmembrane; Repeat; Leucine-rich repeat; Glycoprotein; 3D structure.
 FT SIGNAL 1 18 POTENTIAL.
 FT CHAIN 19 784 TOLL-LIKE RECEPTOR 2.
 FT DOMAIN 19 588 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 589 609 POTENTIAL.
 FT DOMAIN 610 784 CYTOPLASMIC (POTENTIAL).
 FT REPEAT 51 74 LRR 1.
 FT REPEAT 75 98 LRR 2.

REPEAT 99 122 LRR 3. RA Choi S.K., Codani J.J., Conneron I.F., Cummings N.J., Daniel R.A., Denizot F., Devine K.M., Dusterhoff A., Ehrlich S.D., Emerson P.T., FT REPEAT 124 147 LRR 4. RA Denizot F., Devine K.M., Dusterhoff A., Ehrlich S.D., Emerson P.T., FT REPEAT 148 172 LRR 5. RA Entian K.D., Errington J., Fabret C., Ferrari E., Foulger D., FT REPEAT 173 196 LRR 6. RA Fritz C., Fujita M., Fujita Y., Funai S., Galizzi A., Galleron N., FT REPEAT 221 244 LRR 7. RA Ghim S.Y., Glaser P., Goffeau A., Golightly E.J., Grandi G., FT REPEAT 359 384 LRR 8. RA Giuseppi G., Guy B.J., Haga K., Haiech J., Harwood C.R., Renaut A., FT REPEAT 386 411 LRR 9. RA Hilbert H., Holsappel S., Hosono S., Hulio M.F., Itaya M., Jones L., FT REPEAT 412 436 LRR 10. RA Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M., Klein C., FT REPEAT 438 456 LRR 11. RA Kobayashi Y., Koetter P., Koningstein G., Krogh S., Kumano M., FT REPEAT 457 476 LRR 12. RA Kurita K., Lapidus A., Lardinois S., Lauber J., Lazaravic V., FT REPEAT 477 499 LRR 13. RA Lee S.M., Levine A., Liu H., Masuda S., Mauel C., Medigue C., FT REPEAT 501 521 LRR 14. RA Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M., FT DOMAIN 639 784 TIR. RA Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H., FT CARBOHYD 114 114 N-LINKED (GLCNAC. .) (POTENTIAL). RA Parro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M., FT CARBOHYD 199 199 N-LINKED (GLCNAC. .) (POTENTIAL). RA Presecan E., Pujic P., Purnelle B., Rapoport G., Rey M., Reynolds S., FT CARBOHYD 414 414 N-LINKED (GLCNAC. .) (POTENTIAL). RA Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadaie Y., FT CARBOHYD 442 442 N-LINKED (GLCNAC. .) (POTENTIAL). RA Sato T., Scianini E., Schleich S., Schroeter R., Scoffone F., FT MUTAGEN 681 681 P->F: ABOLISHES THE INTERACTION WITH MYD88. NO EFFECT ON OLIGOMERIZATION OR ON THE STRUCTURE OF THE TIR DOMAIN. D -> E (IN REF. 2). RA Sekiguchi J., Sekowska A., Seror S.J., Serror P., Shin B.S., Soldo B., FT CONFLICT 726 726 Score 75; DB 1; Length 784; RA Takeuchi M., Tamakoshi A., Tanaka T., Terpstra P., Tognoni A., FT SEQUENCE 784 AA; 89837 MW; 7DBE6B4C1FAF8B CRC64; RA Tosato V., Uchiyama S., Vandebon M., Vannier F., Vassarotti A., FT SEQUENCE 784 AA; 89837 MW; 7DBE6B4C1FAF8B CRC64; RA Viali A., Wambutt R., Wedler E., Wedler H., Weitzenegger T., FT SEQUENCE 784 AA; 89837 MW; 7DBE6B4C1FAF8B CRC64; RA Winters P., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yata K., FT SEQUENCE 784 AA; 89837 MW; 7DBE6B4C1FAF8B CRC64; RA Yoshida K., Yoshikawa H.F., Zumstein E., Yoshikawa H., Danchin A., RT subtilis. " The complete genome sequence of the gram-positive bacterium Bacillus RT subtilis. " Nature 390:249-256(1997). RL Nature 390:249-256(1997). RN [3]

Qy 21 IFLLFFPSFTGVICTLAITW-----RLKPSADCGRPFRGLPLFIHSIYS----- 64 RP SEQUENCE FROM N.A.

Db 598 LFLLL-LTGVILCHRFHGLWYMMWAWLOAKRKPRK--APSRNICYDAFVSYSERDAY 653 RC SPECIES=Phage SPBc2;

Qy 65 WIDLSTR-----PGYLWVWNTYRNLLGIV--HFFFLTTLIVLI 102 RA Lazarevic V., Duesterhoeft A., Soldo B., Hilbert H., Mauel C., RA Karamata D., R. L. Submitted (AUG-1997) to the EMBL/GenBank/DBJ databases.

Db 654 WVENLWQELENFNPFFKLCIHKRDFIPIG---KWLIDNIDSIKSH---KTVFVISE 705 CC -I- FUNCTION: REQUIRED FOR DISULFIDE BOND FORMATION IN SOME PROTEINS

Qy 103 TYLYWQITEGRKIMRLLHEQIINEGDKMFLIEKLIKQDMEKKANPSSLVLER-- 158 CC -I- SUBCELLULAR LOCATION: Integral membrane protein (Potential).

Db 706 NFKV---SEWCKYELDFSHFLFEDNDAI---LILLEPIEKKAIPORECKLRKIMNT 758 CC -I- SIMILARITY: BELONGS TO THE DSBB FAMILY.

Qy 159 -----EVEQGF 165 CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).

Db 759 KTYLEWPMDEAQREGF 774 CC

RESULT 14

DSBL_BACSU

ID DSBL_BACSU STANDARD; PRT; 148 AA.

AC 064037; 031985; DR EMBL; AF021803; AAC38303.1; -.

DT 16-OCT-2001 (Rel. 40, Created) DR EMBL; Z99115; CAB4062.1; -.

DT 16-OCT-2001 (Rel. 40, Last sequence update) DR Subtilist; BG13587; Yolk.

DT 15-JUN-2002 (Rel. 41, Last annotation update) DR InterPro; IPR003752; DsBB.

DE Putative protein-disulfide oxidoreductase from Spbeta2 prophage. DR Pfam; PF02600; DsB; 1.

GN YOLK. KW Hypothetical protein; oxidoreductase; Redox-active center; OS Bacillus subtilis, and KW Electron transport; Chaperone; Transmembrane.

OS Bacteriophage SPBc2. FT TRANSMEM 8 28 POTENTIAL.

OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus. FT TRANSMEM 65 85 POTENTIAL.

OX NCBI_TaxID=1423, 66797; FT DISULFID 110 130 POTENTIAL.

[1] RN SEQUENCE FROM N.A. FT DISULFID 36 39 REDOX-ACTIVE (BY SIMILARITY).

RP SPECIES=B.subtilis; STRAIN=168; SQ SEQUENCE 148 AA; 17139 MW; 25676A3B9C9AF6DC CRC64;

RX MEDLINE=98240226; PubMed=9579063; RA Regamey A., Karamata D.; RA "The N-acetyl muramoyl-L-alanine amidase encoded by the Bacillus subtilis 168 prophage sp beta.;" RL Microbiology 144:885-893(1998).

RP SEQUENCE FROM N.A. Qy 20 FIFLFFFPSFTGVICTLAITWRLKPSADCGRPFRGLPLFIHSIYSWIDLSTRP-GYLM 77 DR 9 FFLLFFLSEFGTMASLIFYSEIMHFKPCVLC-----WYQRIFLYPIPIIL 53

RC SPECIES=B.subtilis; STRAIN=168; Qy 78 VVWYRNLLGIVFFFILTLIVLILTYW--QITEGRKIMRL 119 DR 54 LIGLKKDLNSIFFVFLSIGLIAYFYIQLTQSWSCEI 97

